

SEQUENCE LISTING

<110> Sheppard, Paul O.
Deisher, Theresa A.
Jaspers, Stephen R.
Bishop, Paul D.

<120> TML Polynucleotides

<130> 97-04D3

<150> 09/404,417

<151> 1999-09-23

<150> 09/046,479

<151> 1998-03-28

<150> 60/041,102

<151> 1997-03-24

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 351

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(351)

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atg ccc tcc cca ggg acc gtc tgc agc ctc ctg ctc ctc ggc atg ctc	48
Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Leu Gly Met Leu	
1 5 10 15	

tgg ctg gac ttg gcc atg gca ggc tcc agc ttc ctg agc cct gaa cac	96
Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro Glu His	
20 25 30	

cag aga gtc cag cag aga aag gag tcg aag aag cca cca gcc aag ctg	144
Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro Ala Lys Leu	
35 40 45	

cag ccc cga gct cta gca ggc tgg ctc cgc ccg gaa gat gga ggt caa	192
Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu Asp Gly Gly Gln	
50 55 60	

gca gaa ggg gca gag gat gaa ctg gaa gtc cgg ttc aac gcc ccc ttt	240
Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg Phe Asn Ala Pro Phe	
65 70 75 80	

gat gtt gga atc aag ctg tca ggg gtt cag tac cag cag cac agc cag	288
Asp Val Gly Ile Lys Leu Ser Gly Val Gln Tyr Gln Gln His Ser Gln	
85 90 95	

gcc ctg ggg aag ttt ctt cag gac atc ctc tgg gaa gag gcc aaa gag	336
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Ala Leu Gly Lys Phe Leu Gln Asp Ile Leu Trp Glu Glu Ala Lys Glu
 100 105 110

gcc cca gcc gac aag
 Ala Pro Ala Asp Lys
 115

351

<210> 2
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 2
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 1 5 10 15
 Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro Glu His
 20 25 30
 Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro Ala Lys Leu
 35 40 45
 Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu Asp Gly Gly Gln
 50 55 60
 Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg Phe Asn Ala Pro Phe
 65 70 75 80
 Asp Val Gly Ile Lys Leu Ser Gly Val Gln Tyr Gln Gln His Ser Gln
 85 90 95
 Ala Leu Gly Lys Phe Leu Gln Asp Ile Leu Trp Glu Glu Ala Lys Glu
 100 105 110
 Ala Pro Ala Asp Lys
 115

<210> 3
 <211> 546
 <212> DNA
 <213> Sus scrofa

<220>
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 <222> (40)...(396)

<400> 3
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 Met Val Ser Arg Lys
 1 5
 gct gtg gtc gtc ctg ctg gtg gtg cac gca gct gcc atg ctg gcc tcc 102
 Ala Val Val Val Leu Leu Val Val His Ala Ala Ala Met Leu Ala Ser
 10 15 20
 cac acg gaa gcc ttt gtt ccc agc ttt acc tac ggg gaa ctt cag agg 150
 His Thr Glu Ala Phe Val Pro Ser Phe Thr Tyr Gly Glu Leu Gln Arg
 25 30 35
 atg cag gaa aag gag cgg aat aaa ggg caa aag aaa tcc ctg agt gtc 198
 Met Gln Glu Lys Glu Arg Asn Lys Gly Gln Lys Lys Ser Leu Ser Val
 40 45 50
 cag cag gcg tcg gag gag ctc ggc cct ctg gac ccc tcg gag ccc acg 246
 Gln Gln Ala Ser Glu Glu Leu Gly Pro Leu Asp Pro Ser Glu Pro Thr
 55 60 65
 aag gaa gaa gaa agg gtg gtt atc aag ctg ctc gcg cct gtg gac att 294

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Lys Glu Glu Glu Arg Val Val Ile Lys Leu Leu Ala Pro Val Asp Ile
 70                      75                      80                      85

gga atc agg atg gac tcc agg cag ctg gaa aag tac cgg gcc acc ctg      342
Gly Ile Arg Met Asp Ser Arg Gln Leu Glu Lys Tyr Arg Ala Thr Leu
                      90                      95                      100

gaa agg ctg ctg ggc cag gcg ccg cag tcc acc cag aac cag aat gcc      390
Glu Arg Leu Leu Gly Gln Ala Pro Gln Ser Thr Gln Asn Gln Asn Ala
                      105                      110                      115

gcc aag taacaggccg ctggggggaga aggaggacac agctcggacc cccctccac      446
Ala Lys

gcagggaggg cctagaaatc cgctgggctt ggaaggaaaa caccctctcc caaacagccc      506
tcagcccccc tccccagca aataaagcgt ggaaataggc      546

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<210> 4
<211> 119
<212> PRT
<213> Sus scrofa

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<400> 4
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Ala Met Leu Ala Ser His Thr Glu Ala Phe Val Pro Ser Phe Thr Tyr
 20          25          30
Gly Glu Leu Gln Arg Met Gln Glu Lys Glu Arg Asn Lys Gly Gln Lys
 35          40          45
Lys Ser Leu Ser Val Gln Gln Ala Ser Glu Glu Leu Gly Pro Leu Asp
 50          55          60
Pro Ser Glu Pro Thr Lys Glu Glu Glu Arg Val Val Ile Lys Leu Leu
 65          70          75          80
Ala Pro Val Asp Ile Gly Ile Arg Met Asp Ser Arg Gln Leu Glu Lys
 85          90          95
Tyr Arg Ala Thr Leu Glu Arg Leu Leu Gly Gln Ala Pro Gln Ser Thr
100          105          110
Gln Asn Gln Asn Ala Ala Lys
115

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<210> 5
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<212> PRT
<213> Artificial Sequence

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<220>
<223> Artificial peptide

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<221> VARIANT
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<221> VARIANT
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<221> VARIANT
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1 5

<210> 6

<211> 7

<212> PRT

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<223> Xaa = Any Amino Acid

<221> VARIANT

<222> (1)...(7)

<223> Xaa = Any Amino Acid

<400> 6

Ala Pro Xaa Asp Xaa Gly Ile
1 5

<210> 7

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 7

ttcttcgact cctttctctg ctggactctc tgggtgttcag

40

<210> 8

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 8

catgctctgg ctggactt

18

<210> 9

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 9
ctggactctc tgggtgttc 18

<210> 10
<211> 54
<212> DNA
<213> Homo sapiens

<400> 10
ggctccagct tcctgagccc tgaacaccag agagtccagc agagaaagga gtcg 54

<210> 11
<211> 18
<212> PRT
<213> Homo sapiens

<400> 11
Gly Ser Ser Phe Leu Ser Pro Glu His Gln Arg Val Gln Gln Arg Lys
1 5 10 15
Glu Ser

<210> 12
<211> 18
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<223> Xaa is Gly, Ser, Ala, Thr, or Met

<221> VARIANT
<222> (2)...(2)
<223> Xaa is Gly, Ser, Ala, Thr, or Met

<221> VARIANT
<222> (3)...(3)
<223> Xaa is Gly, Ser, Ala, Thr, or Met

<221> VARIANT
<222> (4)...(4)
<223> Xaa is Phe, Trp, Tyr, Leu, Val, or Ile

<221> VARIANT
<222> (5)...(5)
<223> Xaa is Phe, Tyr, Leu, Val, or Ile

<221> VARIANT
<222> (6)...(6)
<223> Xaa is Gly, Ser, Ala, Thr, Met, or Pro

<221> VARIANT
<222> (7)...(7)
<223> Xaa is Gly, Pro, Ala, Ile, leu or Val

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<223> Xaa is Glu or Asp

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<223> Xaa is His, Arg, Lys, Phe, or Tyr

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<223> Xaa is Gln, Asn, Ser, Thr, His, Ala, Glu, Asp,
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<221> VARIANT
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<221> VARIANT
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<223> Xaa is Gln, Asn, Ser, Thr, His, Ala, Glu, Asp,
      Lys, or Arg

<400> 12
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1           5           10           15
Xaa Xaa

<210> 13
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial peptide

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<400> 13

Ser Leu Ser Arg Gln Gly Ser His Gln Phe Pro Gln Glu Val
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